

09/357709
Docket 242/026
Express Mail
EL199138787WS

LQM

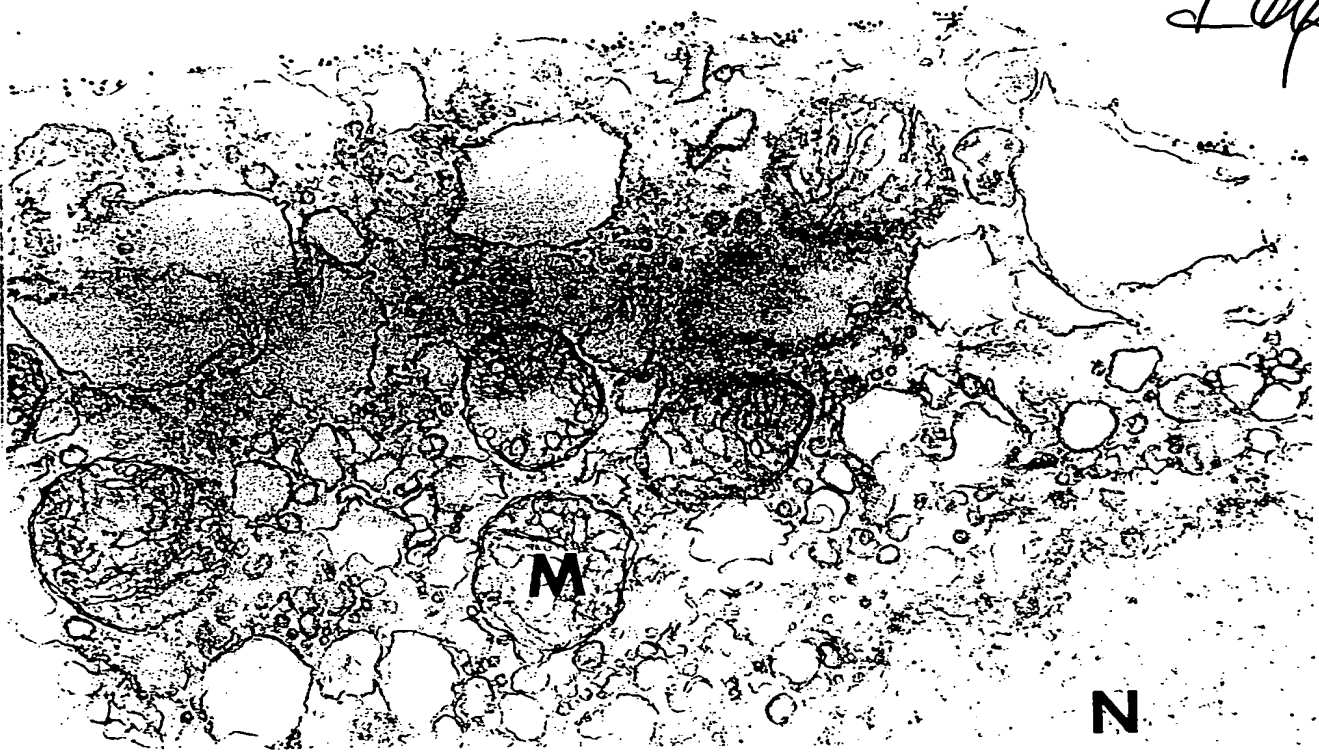
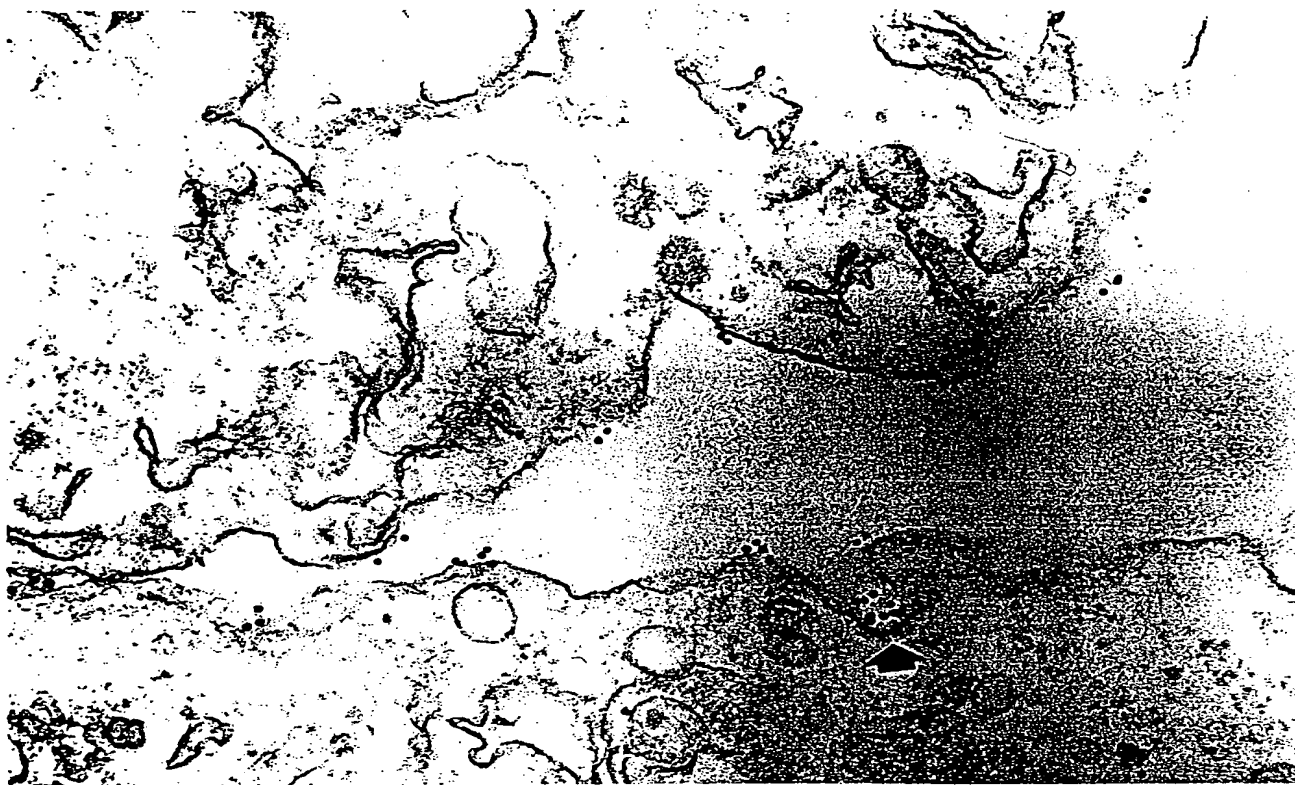


FIGURE 1



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660220" 6074560

FIGURE 2

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FIGURE 3

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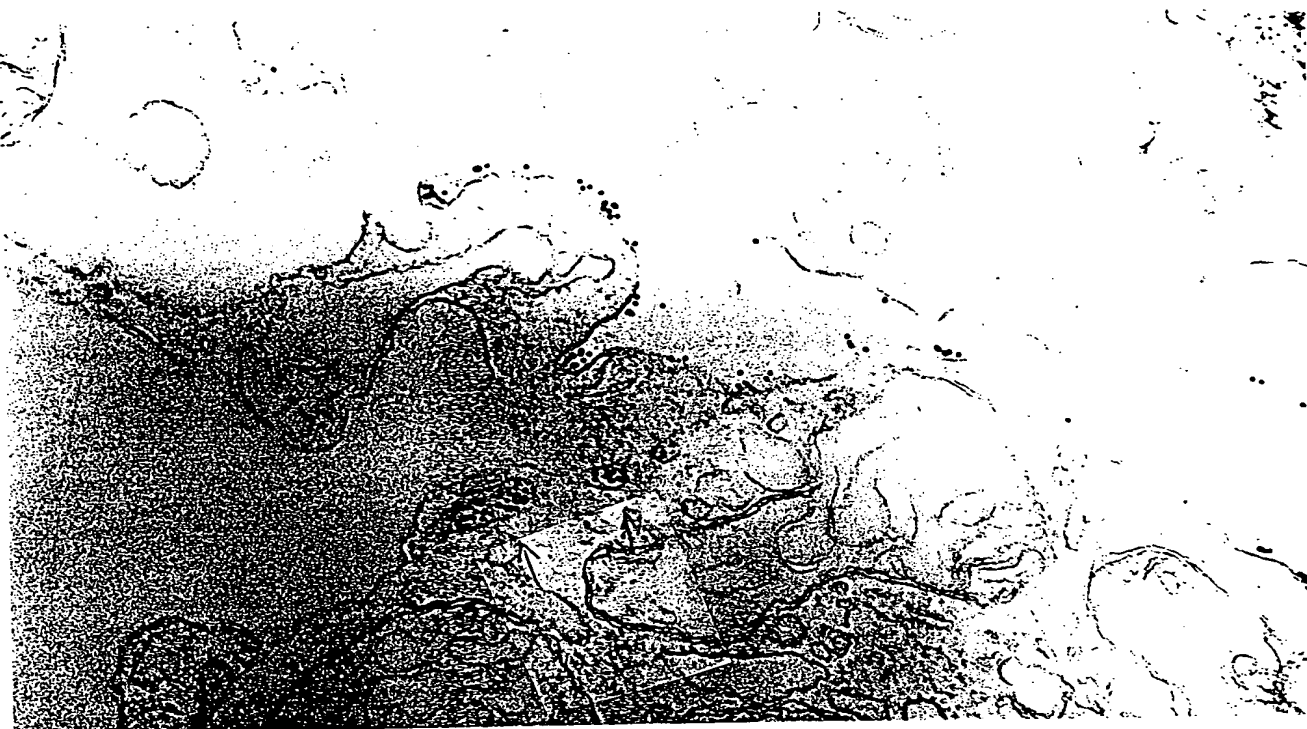


FIGURE 4



FIGURE 5

6602/0" 60/4850

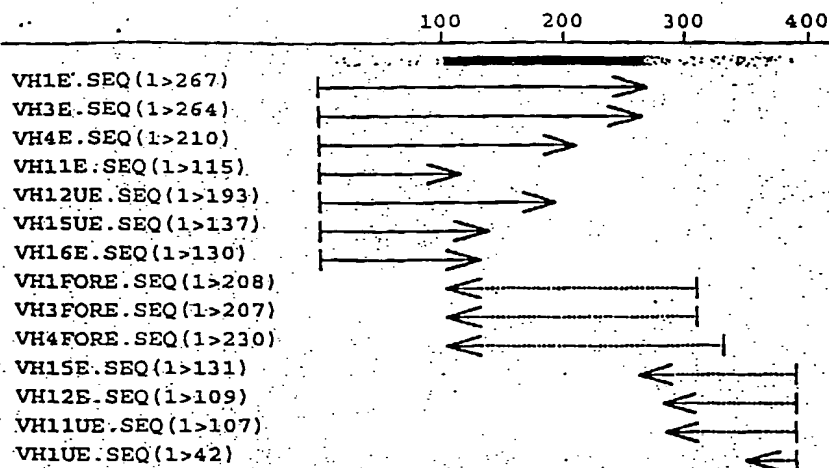


FIGURE 6

Enzymes : All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

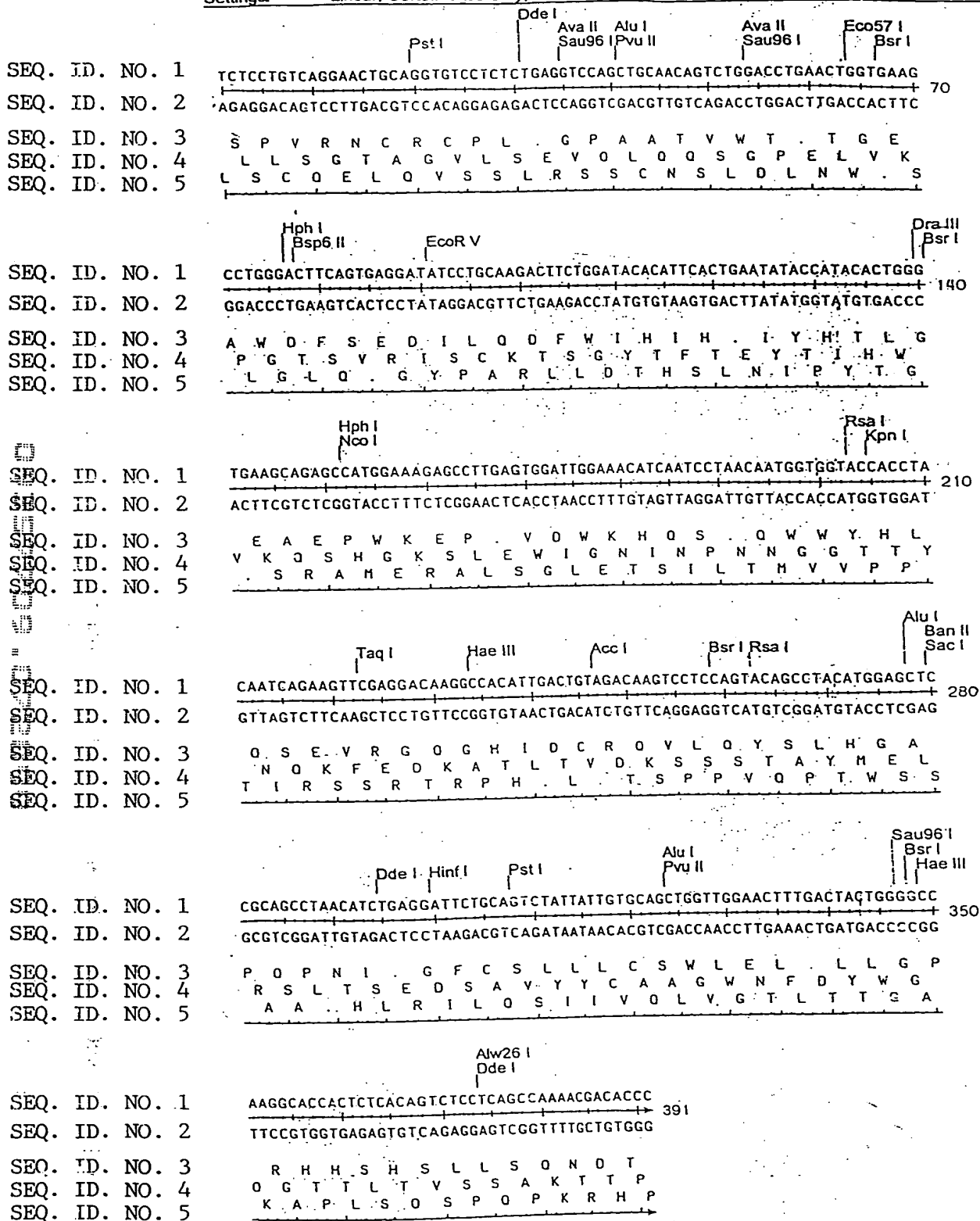


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

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      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKQSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
60      70      80      90      100     110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGT
YNQKF :KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ...FDYWGQGT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGT
      70      80      90      100     110     120

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LTVSS
:TVSS
VTVSS

FIGURE 8

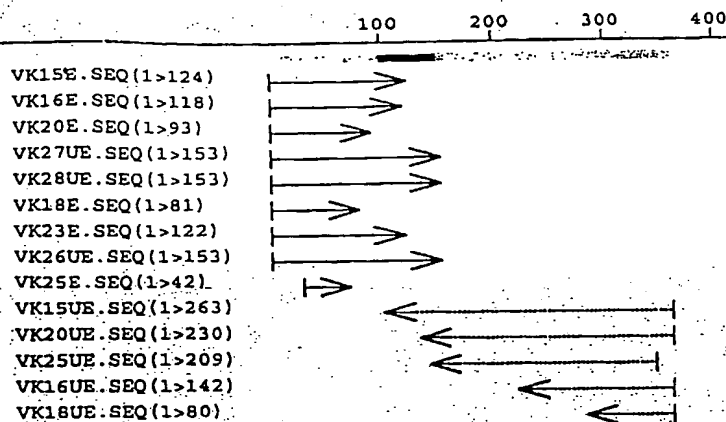


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

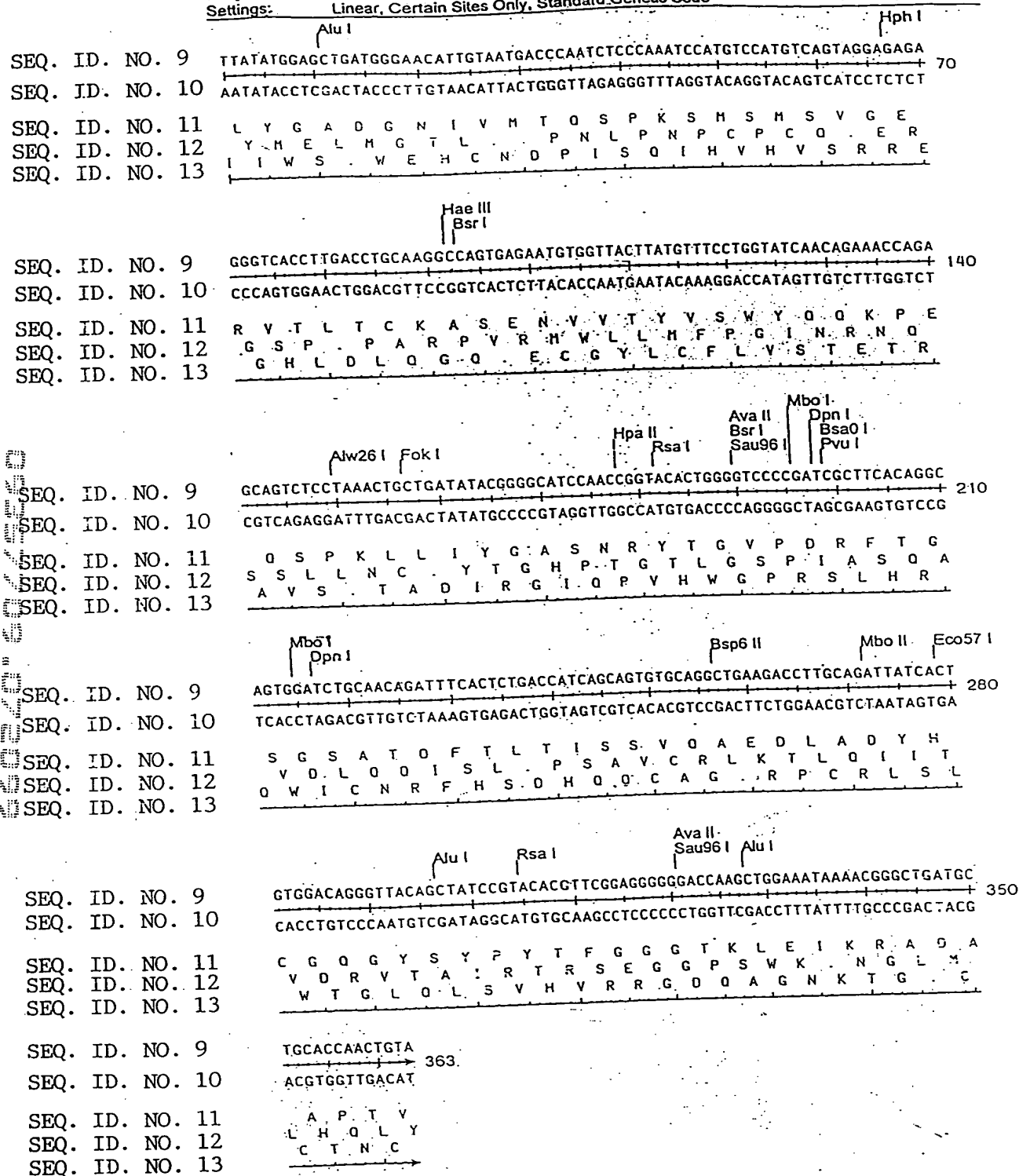


FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO	60.4	2	2	109

(1>107)	(1>109)	60.4	2	2	109
✓10	✓20	✓30	✓40	✓50	
NIVMTQSPKSMMSGVGERVTLTCKAS-ENVVTTYVSWYQQKPEQSPKLLIYGASNRYTGVP					
:I MTQSP.S:S S:G:RVT:TC:AS :::Y::WYQQK. SPKLLIY AS. :GVP					
DIOMTQSPSSLSASLGDRVTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP					
^10	^20	^30	^40	^50	^60
✓60	✓70	✓80	✓90	✓100	
DRFTGSGSATDFTLTISSVOAEDLADYHCGQGYSY-PYTFGGGKLEIK					
RF:GSGS:TD::LTIS:::ED:A.Y C.QG::P TFGGGKLEIK					
SRFSGSGSGTDYSLTISNLEQEDLATYFCQQGNTLPPRTFGGGKLEIK					
^70	^80	^90	^100		

FIGURE 11